

SEQUENCE LISTING

<110> De Sauvage, Frederic J.
Klein, Richard D.
Rosenthal, Arnon
Phillips, Heidi S.

<120> GFRALPHA3 AND ITS USES

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<150> 60/079,124
<151> 1998-03-23

<150> 60/081,569
<151> 1998-04-13

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<213> Mus musculus

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gtcttagaag tgagggtctgt gacccttccg atccgtagcg gctagtttc aaacccctccct 180
tgccccctgtc tccttctggc tcaggctgtc cctccttagg actttgtggg tccagtttg 240
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<211> 353
<212> DNA
<213> Mus musculus

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ccacttggag cagggaaactc cttggccaca gagaacaggt ttgtgaacag ctgtacccag 180
gccagaaaaga aatgcgaggc taatcccgct tgcaaggctg cttaccagca cctgggctcc 240
tgcacccctca gttaagcagg ccgctgcct tagaggagtc tgccatgtct gcagactgcc 300
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<211> 498
<212> DNA
<213> Mus musculus

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agtgggactc cgacacaatgt gaagaacacgc tggaaagagac catcaaaaac tgcctgtctg 180
cagcagagga caagaagctt aaatccgtcg cttcccaacc gttccccagt ggcagaaact 240
gttcccaa acagacggcc gcccaggtga ccctcaaggg catctcggt cacttcgacg 300
actcgagctc gtccctcgctg aagaatgtgt acttcctgtc cttcgacagc gagacatcg 360
catctacgtc caggagatgg ccaaactggc caccaagtgc ctctctccag tggccggcggaa 420
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<210> 4

<211> 1935

<212> DNA

<213> *Mus musculus*

<400> 4

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gaacagctct ctgatagact gcaggtgcca tcggcgcatg aagcacaag ctacctgtct 420
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<210> 5

<211> 397

<212> PRT

<213> *Mus musculus*

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 Thr Glu Asn Arg Phe Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys
 35 40 45
 Glu Ala Asn Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Gly Ser Cys
 50 55 60
 Thr Ser Ser Leu Ser Arg Pro Leu Pro Leu Glu Glu Ser Ala Met Ser
 65 70 75 80
 Ala Asp Cys Leu Glu Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile
 85 90 95
 Asp Cys Arg Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp
 100 105 110
 Ile Tyr Trp Thr Val His Pro Ala Arg Ser Leu Gly Asp Tyr Glu Leu
 115 120 125
 Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro Trp Lys Met
 130 135 140
 Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp Leu Cys Leu
 145 150 155 160
 Lys Phe Ala Met Leu Cys Thr Leu His Asp Lys Cys Asp Arg Leu Arg
 165 170 175
 Lys Ala Tyr Gly Glu Ala Cys Ser Gly Ile Arg Cys Gln Arg His Leu
 180 185 190
 Cys Leu Ala Gln Leu Arg Ser Phe Phe Glu Lys Ala Ala Glu Ser His
 195 200 205
 Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Glu Asp Ala Gly Cys
 210 215 220
 Gly Glu Arg Arg Arg Asn Thr Ile Ala Pro Ser Cys Ala Leu Pro Ser
 225 230 235 240
 Val Thr Pro Asn Cys Leu Asp Leu Arg Ser Phe Cys Arg Ala Asp Pro
 245 250 255
 Leu Cys Arg Ser Arg Leu Met Asp Phe Gln Thr His Cys His Pro Met
 260 265 270
 Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys Leu Arg Ala
 275 280 285
 Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe Ile Ser Lys
 290 295 300
 Val Asn Thr Thr Val Ala Leu Ser Cys Thr Cys Arg Gly Ser Gly Asn
 305 310 315 320
 Leu Gln Asp Glu Cys Glu Gln Leu Glu Arg Ser Phe Ser Gln Asn Pro
 325 330 335
 Cys Leu Val Glu Ala Ile Ala Ala Lys Met Arg Phe His Arg Gln Leu
 340 345 350
 Phe Ser Gln Asp Trp Ala Asp Ser Thr Phe Ser Val Val Gln Gln Gln
 355 360 365
 Asn Ser Asn Pro Ala Leu Arg Leu Gln Pro Arg Leu Pro Ile Leu Ser
 370 375 380
 Phe Ser Ile Leu Pro Leu Ile Leu Leu Gln Thr Leu Trp
 385 390 395

<210> 6
 <211> 460
 <212> PRT
 <213> Homo sapiens

<400> 6

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35 40 45
Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Ala Ser
50 55 60
Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
65 70 75 80
Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
85 90 95
Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
100 105 110
Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
115 120 125
Ser Asp Ile Phe Arg Val Val Pro Phe Ile Ser Val Glu His Ile Pro
130 135 140
Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asp Asp
145 150 155 160
Ile Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr Pro Cys Thr Thr Ser
165 170 175
Val Ser Asn Asp Val Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg
180 185 190
Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser Tyr Gly Met Leu Phe
195 200 205
Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg Arg Arg Gln Thr Ile
210 215 220
Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Lys Pro Asn Cys Leu Asn
225 230 235 240
Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys Arg Ser Arg Leu Ala
245 250 255
Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg Ser Val Ser Ser Cys
260 265 270
Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala Tyr Ser Gly Leu Ile
275 280 285
Gly Thr Val Met Thr Pro Asn Tyr Ile Asp Ser Ser Leu Ser Val
290 295 300
Ala Pro Trp Cys Asp Cys Ser Asn Ser Gly Asn Asp Leu Glu Glu Cys
305 310 315 320
Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr Cys Leu Lys Asn Ala
325 330 335
Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr Val Trp Gln Pro Ala
340 345 350
Phe Pro Val Gln Thr Thr Ala Thr Thr Thr Ala Leu Arg Val
355 360 365
Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu Asn Glu Ile Pro Thr
370 375 380
His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala Gln Lys Leu Lys Ser
385 390 395 400
Asn Val Ser Gly Asn Thr His Leu Cys Ile Ser Asn Gly Asn Tyr Glu
405 410 415
Lys Glu Gly Leu Gly Ala Ser Ser His Ile Thr Thr Lys Ser Met Ala
420 425 430
Ala Pro Pro Ser Cys Gly Leu Ser Pro Leu Leu Val Leu Val Val Thr

435 440 445
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450 455 460

<210> 7
<211> 464
<212> PRT
<213> Homo sapiens

<400> 7
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Gly Trp Arg Pro Pro Val Asp Cys Val Arg Ala Asn Glu Leu Cys Ala
35 40 45
Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu
50 55 60
Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala
65 70 75 80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys
85 90 95
Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile
100 105 110
His Leu Gly Leu Thr Glu Gly Glu Phe Tyr Glu Ala Ser Pro Tyr
115 120 125
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile
130 135 140
Phe Ser Gly Thr Gly Ala Asp Pro Val Val Ser Ala Lys Ser Asn His
145 150 155 160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys
165 170 175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr
180 185 190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe
195 200 205
Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser Cys
210 215 220
Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro Ser
225 230 235 240
Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg Gly
245 250 255
Val Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe His
260 265 270
Ala Asn Cys Arg Ala Ser Tyr Gln Thr Val Thr Ser Cys Pro Ala Asp
275 280 285
Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe Asp
290 295 300
Met Thr Pro Asn Tyr Val Asp Ser Ser Pro Thr Gly Ile Val Val Ser
305 310 315 320
Pro Trp Cys Ser Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys Glu
325 330 335
Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala Ile
340 345 350
Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Val Ser Pro Lys Gly Pro
355 360 365

Ser Phe Gln Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser Leu
 370 375 380
 Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile Thr
 385 390 395 400
 Thr Cys Thr Ser Val Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser Lys
 405 410 415
 Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro Gly
 420 425 430
 Ser Asn Lys Val Ile Lys Pro Asn Ser Gly Pro Ser Arg Ala Arg Pro
 435 440 445
 Ser Ala Ala Leu Thr Val Leu Ser Val Leu Met Leu Lys Leu Ala Leu
 450 455 460

<210> 8
 <211> 468
 <212> PRT
 <213> Rattus norvegicus

<400> 8
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 35 40 45
 Leu Arg Gln Cys Val Ala Gly Lys Glu Thr Asn Phe Ser Leu Thr Ser
 50 55 60
 Gly Leu Glu Ala Lys Asp Glu Cys Arg Ser Ala Met Glu Ala Leu Lys
 65 70 75 80
 Gln Lys Ser Leu Tyr Asn Cys Arg Cys Lys Arg Gly Met Lys Lys Glu
 85 90 95
 Lys Asn Cys Leu Arg Ile Tyr Trp Ser Met Tyr Gln Ser Leu Gln Gly
 100 105 110
 Asn Asp Leu Leu Glu Asp Ser Pro Tyr Glu Pro Val Asn Ser Arg Leu
 115 120 125
 Ser Asp Ile Phe Arg Ala Val Pro Phe Ile Ser Asp Val Phe Gln Gln
 130 135 140
 Val Glu His Ile Ser Lys Gly Asn Asn Cys Leu Asp Ala Ala Lys Ala
 145 150 155 160
 Cys Asn Leu Asp Asp Thr Cys Lys Lys Tyr Arg Ser Ala Tyr Ile Thr
 165 170 175
 Pro Cys Thr Thr Ser Met Ser Asn Glu Val Cys Asn Arg Arg Lys Cys
 180 185 190
 His Lys Ala Leu Arg Gln Phe Phe Asp Lys Val Pro Ala Lys His Ser
 195 200 205
 Tyr Gly Met Leu Phe Cys Ser Cys Arg Asp Ile Ala Cys Thr Glu Arg
 210 215 220
 Arg Arg Gln Thr Ile Val Pro Val Cys Ser Tyr Glu Glu Arg Glu Arg
 225 230 235 240
 Pro Asn Cys Leu Ser Leu Gln Asp Ser Cys Lys Thr Asn Tyr Ile Cys
 245 250 255
 Arg Ser Arg Leu Ala Asp Phe Phe Thr Asn Cys Gln Pro Glu Ser Arg
 260 265 270
 Ser Val Ser Asn Cys Leu Lys Glu Asn Tyr Ala Asp Cys Leu Leu Ala
 275 280 285
 Tyr Ser Gly Leu Ile Gly Thr Val Met Thr Pro Asn Tyr Val Asp Ser

290	295	300
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305	310	315
Asp Leu Glu Asp Cys Leu Lys Phe Leu Asn Phe Phe Lys Asp Asn Thr		320
325	330	335
Cys Leu Lys Asn Ala Ile Gln Ala Phe Gly Asn Gly Ser Asp Val Thr		
340	345	350
Met Trp Gln Pro Ala Pro Pro Val Gln Thr Thr Ala Thr Thr Thr		
355	360	365
Thr Ala Phe Arg Val Lys Asn Lys Pro Leu Gly Pro Ala Gly Ser Glu		
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Asn Glu Ile Pro Thr His Val Leu Pro Pro Cys Ala Asn Leu Gln Ala		
385	390	395
Gln Lys Leu Lys Ser Asn Val Ser Gly Ser Thr His Leu Cys Leu Ser		400
405	410	415
Asp Ser Asp Phe Gly Lys Asp Gly Leu Ala Gly Ala Ser Ser His Ile		
420	425	430
Thr Thr Lys Ser Met Ala Ala Pro Pro Ser Cys Ser Leu Ser Ser Leu		
435	440	445
Pro Val Leu Met Leu Thr Ala Leu Ala Ala Leu Leu Ser Val Ser Leu		
450	455	460
Ala Glu Thr Ser		
465		

<210> 9
 <211> 464
 <212> PRT
 <213> Rattus Norvegicus

<400> 9			
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Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys Leu			
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Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln Ala			
65	70	75	80
Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys Lys			
85	90		95
Arg Gly Met Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser Ile			
100	105	110	
His Leu Gly Leu Thr Glu Gly Glu Phe Tyr Glu Ala Ser Pro Tyr			
115	120	125	
Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser Ile			
130	135	140	
Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn His			
145	150	155	160
Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys Lys			
165	170		175
Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro Thr			
180	185		190
Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe Phe			
195	200	205	

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225					230					235					240
Cys	Ser	Tyr	Glu	Asp	Lys	Glu	Lys	Pro	Asn	Cys	Leu	Asp	Leu	Arg	Ser
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Pro	Trp	Cys	Asn	Cys	Arg	Gly	Ser	Gly	Asn	Met	Glu	Glu	Glu	Cys	Glu
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Lys	Phe	Leu	Arg	Asp	Phe	Thr	Glu	Asn	Pro	Cys	Leu	Arg	Asn	Ala	Ile
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Ser	Leu	Pro	Ala	Thr	Gln	Ala	Pro	Arg	Val	Glu	Lys	Thr	Pro	Ser	Leu
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Pro	Asp	Asp	Leu	Ser	Asp	Ser	Thr	Ser	Leu	Gly	Thr	Ser	Val	Ile	Thr
385				390					395						400
Thr	Cys	Thr	Ser	Ile	Gln	Glu	Gln	Gly	Leu	Lys	Ala	Asn	Asn	Ser	Lys
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Glu	Leu	Ser	Met	Cys	Phe	Thr	Glu	Leu	Thr	Thr	Asn	Ile	Ser	Pro	Gly
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Ser	Lys	Lys	Val	Ile	Lys	Leu	Asn	Ser	Gly	Ser	Ser	Arg	Ala	Arg	Leu
			435			440					445				
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<212> DNA
<213> *Homo sapiens*

<220>

<221> unsure
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<223> n = A, T, C or G

<400> 10

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nnnnnnnnngc	ctctcgacgc	cggagacccc	cttcccacag	aaagccgact	catgaacagc	240
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<211> 20

<212> DNA

<213> Homo sapiens

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tcgtctccctc ctctgagtttgg aggtggaaa actactgcct gcactgcctt gtcggggat 1680		
cctgcccgaac atctgggcattt caggagctgg agcctgtggg ctttgcttta ttcttattat 1740		
tgtcctaaag tctctcttggg ctcttggatc atgattaaac ctttgactta ag		1792
<210> 15		

<211> 400
<212> PRT
<213> Homo Sapiens

<400> 15
Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1 5 10 15
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20 25 30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35 40 45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
50 55 60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65 70 75 80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85 90 95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala
100 105 110
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser Leu Gly Asn
115 120 125
Tyr Glu Leu Asp Val Ser Pro Tyr Glu Asp Thr Val Thr Ser Lys Pro
130 135 140
Trp Lys Met Asn Leu Ser Lys Leu Asn Met Leu Lys Pro Asp Ser Asp
145 150 155 160
Leu Cys Leu Lys Phe Ala Met Leu Cys Thr Leu Asn Asp Lys Cys Asp
165 170 175
Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser Gly Pro His Cys Gln
180 185 190
Arg His Val Cys Leu Arg Gln Leu Leu Thr Phe Phe Glu Lys Ala Ala
195 200 205
Glu Pro His Ala Gln Gly Leu Leu Leu Cys Pro Cys Ala Pro Asn Asp
210 215 220
Arg Gly Cys Gly Glu Arg Arg Asn Thr Ile Ala Pro Asn Cys Ala
225 230 235 240
Leu Pro Pro Val Ala Pro Asn Cys Leu Glu Leu Arg Arg Leu Cys Phe
245 250 255
Ser Asp Pro Leu Cys Arg Ser Arg Leu Val Asp Phe Gln Thr His Cys
260 265 270
His Pro Met Asp Ile Leu Gly Thr Cys Ala Thr Glu Gln Ser Arg Cys
275 280 285
Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr Ala Met Thr Pro Asn Phe
290 295 300
Val Ser Asn Val Asn Thr Ser Val Ala Leu Ser Cys Thr Cys Arg Gly
305 310 315 320
Ser Gly Asn Leu Gln Glu Glu Cys Glu Met Leu Glu Gly Phe Phe Ser
325 330 335
His Asn Pro Cys Leu Thr Glu Ala Ile Ala Ala Lys Met Arg Phe His
340 345 350
Ser Gln Leu Phe Ser Gln Asp Trp Pro His Pro Thr Phe Ala Val Met
355 360 365
Ala His Gln Asn Glu Asn Pro Ala Val Arg Pro Gln Pro Trp Val Pro
370 375 380
Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile Leu Leu Ser Leu Trp
385 390 395 400

<210> 16
<211> 1837
<212> DNA
<213> Homo sapeins

<400> 16
ccaggagacc tggtggaga gtgtgtgcgt cgcgctggag ggccggaggc gggggcggga 60
ggtgcgggtc gagggagccc cgctctcaga gctccagggg aggagcagg ggagcgcggga 120
gccccggcgc tacagctcgc catggtgcgc cccctgaacc cgcgaccgct gccgcccgt 180
gtcctgatgt tgctgctgct gctgccggc tcgcccgtc ctctcgacg cggagacccc 240
cttcccacag aaaggcact catgaacacgc tgtctccagg ccaggagaa gtgccaggct 300
gatcccacct gcagtgcgtc ctaccaccac ctggattcct gcacctctag cataagcacc 360
ccactgcctc cagaggagcc ttccggccct gctgactgccc tggaggcagc acagcaactc 420
aggaacagct ctctgatagg ctgcattgtc caccggcga tgaagaacca ggttgcctgc 480
ttggacatct attggaccgt tcaccgtgcc cgacgcctt actcagacct ctgcctcaag 540
tttgccatgc tgttactct caatgacaag tgtgaccggc tgcgcacggc ctacggggag 600
gcgtgcgtcg gcccccaactg ccagcgccac gtctgcctca ggcagctgtc cactttctc 660
gagaaggcgc ccgagcccca cgccgcaggcgt ctgtactgt gccccatgtc ccccaacgc 720
cggggctgcg gggagcgcgcg ggcacacacc atgccccca actgcgcgtc gccgcctgt 780
gcccccaact gcctggagct gccggcgcctc tgcttctccg acccgctttg cagatcacgc 840
ctggtgatt tccagaccca ctgcattccc atggacatcc taggaacttg tgcacacagag 900
cagtccagat gtctacgagc atacctgggg ctgattggga ctgcattgac ccccaactt 960
gtcagcaatg tcaacaccag tggcctta agctgcaccc ggcaggcag tggcaacctg 1020
caggaggagt gtgaaatgct ggaagggttc ttctccaca acccctgcct cacggaggcc 1080
attgcagctc agatgcgtt tcacagccaa ctcttctccc aggactggcc acaccctacc 1140
tttgctgtga tggcacacca gaatgaaaac cctgctgtga ggcacagcc ctgggtgccc 1200
tctctttct cctgcacgc tcccttgatt ctgcctctga gcctatgtt gctggacttc 1260
cccaggccccc tctttccctc caccacaccc aggtggactt gcagccacca aggggtgagg 1320
aaaggacagc agcaggaagg aggtgcagtgc cgcagatgag ggcacaggag aagctaagg 1380
ttatgaccc cagatccctt ctggtccagt cctcattccc tccacccat ctccacttct 1440
gattcatgt gcccctccctt ggtggccaca atttagccat gtcattgtt ggtgaccagc 1500
tccaccaagc cccttctga gcccctccctt ttgactacca ggatcaccag aatctaataa 1560
gttagcctt ctctattgca ttccagatgg gggtagggt agggaggact ggggtttctg 1620
aggcagccata gaaagtatttcttgc aagaaggctc ctgcctccctc gtctcctcct 1680
ctgagtgag gatgaaaac tactgcgtc actgcctgt ccccgatcc tgcgaacat 1740
ctgggcatac ggagctggag cctgtggcc ttgctttatt cctattatttgc tcctaaagtc 1800
tctctgggctt ctggatcat gattaaacct ttgactt 1837

<210> 17
<211> 369
<212> PRT
<213> Homo sapiens

<400> 17
Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
1 5 10 15
Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
20 25 30
Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
35 40 45
Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
50 55 60
Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
65 70 75 80
Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser
85 90 95
Ser Leu Ile Gly Cys Met Cys His Arg Arg Met Lys Asn Gln Val Ala

100	105	110	
Cys Leu Asp Ile Tyr Trp Thr Val His Arg Ala Arg Ser	Leu Asp Ser		
115	120	125	
Asp Leu Cys Leu Lys Phe Ala Met Leu Cys Thr	Leu Asn Asp Lys Cys		
130	135	140	
Asp Arg Leu Arg Lys Ala Tyr Gly Glu Ala Cys Ser	Gly Pro His Cys		
145	150	155	160
Gln Arg His Val Cys Leu Arg Gln Leu Leu Thr	Phe Phe Glu Lys Ala		
165	170	175	
Ala Glu Pro His Ala Gln Gly Leu Leu Cys Pro	Cys Ala Pro Asn		
180	185	190	
Asp Arg Gly Cys Gly Glu Arg Arg Asn Thr	Ile Ala Pro Asn Cys		
195	200	205	
Ala Leu Pro Pro Val Ala Pro Asn Cys Leu Glu	Leu Arg Arg Leu Cys		
210	215	220	
Phe Ser Asp Pro Leu Cys Arg Ser Arg Leu Val	Asp Phe Gln Thr His		
225	230	235	240
Cys His Pro Met Asp Ile Leu Gly Thr Cys Ala	Thr Glu Gln Ser Arg		
245	250	255	
Cys Leu Arg Ala Tyr Leu Gly Leu Ile Gly Thr	Ala Met Thr Pro Asn		
260	265	270	
Phe Val Ser Asn Val Asn Thr Ser Val Ala Leu	Ser Cys Thr Cys Arg		
275	280	285	
Gly Ser Gly Asn Leu Gln Glu Glu Cys Glu Met	Leu Glu Gly Phe Phe		
290	295	300	
Ser His Asn Pro Cys Leu Thr Glu Ala Ile Ala	Ala Lys Met Arg Phe		
305	310	315	320
His Ser Gln Leu Phe Ser Gln Asp Trp Pro His	Pro Thr Phe Ala Val		
325	330	335	
Met Ala His Gln Asn Glu Asn Pro Ala Val Arg	Pro Gln Pro Trp Val		
340	345	350	
Pro Ser Leu Phe Ser Cys Thr Leu Pro Leu Ile	Leu Leu Ser Leu		
355	360	365	
Trp			

<210> 18
 <211> 628
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric receptor comprising human sequence.

<400> 18
 Met Val Arg Pro Leu Asn Pro Arg Pro Leu Pro Pro Val Val Leu Met
 1 5 10 15
 Leu Leu Leu Leu Pro Pro Ser Pro Leu Pro Leu Ala Ala Gly Asp
 20 25 30
 Pro Leu Pro Thr Glu Ser Arg Leu Met Asn Ser Cys Leu Gln Ala Arg
 35 40 45
 Arg Lys Cys Gln Ala Asp Pro Thr Cys Ser Ala Ala Tyr His His Leu
 50 55 60
 Asp Ser Cys Thr Ser Ser Ile Ser Thr Pro Leu Pro Ser Glu Glu Pro
 65 70 75 80
 Ser Val Pro Ala Asp Cys Leu Glu Ala Ala Gln Gln Leu Arg Asn Ser

	85	90	95												
Ser	Leu	Ile	Gly	Cys	Met	Cys	His	Arg	Arg	Met	Lys	Asn	Gln	Val	Ala
	100						105				110				
Cys	Leu	Asp	Ile	Tyr	Trp	Thr	Val	His	Arg	Ala	Arg	Ser	Leu	Gly	Asn
	115						120				125				
Tyr	Glu	Leu	Asp	Val	Ser	Pro	Tyr	Glu	Asp	Thr	Val	Thr	Ser	Lys	Pro
	130					135				140					
Trp	Lys	Met	Asn	Leu	Ser	Lys	Leu	Asn	Met	Leu	Lys	Pro	Asp	Ser	Asp
	145					150				155			160		
Leu	Cys	Leu	Lys	Phe	Ala	Met	Leu	Cys	Thr	Leu	Asn	Asp	Lys	Cys	Asp
						165			170			175			
Arg	Leu	Arg	Lys	Ala	Tyr	Gly	Glu	Ala	Cys	Ser	Gly	Pro	His	Cys	Gln
						180		185			190				
Arg	His	Val	Cys	Leu	Arg	Gln	Leu	Leu	Thr	Phe	Phe	Glu	Lys	Ala	Ala
						195		200			205				
Glu	Pro	His	Ala	Gln	Gly	Leu	Leu	Leu	Cys	Pro	Cys	Ala	Pro	Asn	Asp
						210		215			220				
Arg	Gly	Cys	Gly	Glu	Arg	Arg	Arg	Asn	Thr	Ile	Ala	Pro	Asn	Cys	Ala
						225		230			235			240	
Leu	Pro	Pro	Val	Ala	Pro	Asn	Cys	Leu	Glu	Leu	Arg	Arg	Leu	Cys	Phe
						245			250			255			
Ser	Asp	Pro	Leu	Cys	Arg	Ser	Arg	Leu	Val	Asp	Phe	Gln	Thr	His	Cys
						260			265			270			
His	Pro	Met	Asp	Ile	Leu	Gly	Thr	Cys	Ala	Thr	Glu	Gln	Ser	Arg	Cys
						275			280			285			
Leu	Arg	Ala	Tyr	Leu	Gly	Leu	Ile	Gly	Thr	Ala	Met	Thr	Pro	Asn	Phe
						290		295			300				
Val	Ser	Asn	Val	Asn	Thr	Ser	Val	Ala	Leu	Ser	Cys	Thr	Cys	Arg	Gly
						305		310			315			320	
Ser	Gly	Asn	Leu	Gln	Glu	Glu	Cys	Glu	Met	Leu	Glu	Gly	Phe	Phe	Ser
						325			330			335			
His	Asn	Pro	Cys	Leu	Thr	Glu	Ala	Ile	Ala	Ala	Lys	Met	Arg	Phe	His
						340			345			350			
Ser	Gln	Leu	Phe	Ser	Gln	Asp	Trp	Pro	His	Pro	Thr	Phe	Ala	Val	Met
						355			360			365			
Ala	His	Gln	Asn	Glu	Asn	Pro	Ala	Val	Arg	Pro	Gln	Pro	Trp	Val	Pro
						370		375			380				
Ser	Leu	Phe	Ser	Cys	Thr	Leu	Pro	Leu	Ile	Leu	Leu	Leu	Ser	Leu	Trp
						385		390			395			400	
Pro	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu
						405			410			415			
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu
						420			425			430			
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser
						435			440			445			
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu
						450			455			460			
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr
						465			470			475			480
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn
						485			490			495			
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro
						500			505			510			
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln
						515			520			525			
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val
						530			535			540			

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
545 550 555 560
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
565 570 575
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
580 585 590
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
595 600 605
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
610 615 620
Ser Pro Gly Lys
625

<210> 19
<211> 951
<212> PRT
<213> Artificial Sequence

<220>
<223> Chimeric receptor comprising rat sequence.

<400> 19
Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
1 5 10 15
Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala
20 25 30
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
35 40 45
Val Leu Asp Gln Leu Leu Glu Pro Ser Ser Leu Gln Gly Ser Glu Leu
50 55 60
His Gly Trp Arg Pro Gln Val Asp Cys Val Arg Ala Asn Glu Leu Cys
65 70 75 80
Ala Ala Glu Ser Asn Cys Ser Ser Arg Tyr Arg Thr Leu Arg Gln Cys
85 90 95
Leu Ala Gly Arg Asp Arg Asn Thr Met Leu Ala Asn Lys Glu Cys Gln
100 105 110
Ala Ala Leu Glu Val Leu Gln Glu Ser Pro Leu Tyr Asp Cys Arg Cys
115 120 125
Lys Arg Gly Met Lys Lys Glu Leu Gln Cys Leu Gln Ile Tyr Trp Ser
130 135 140
Ile His Leu Gly Leu Thr Glu Gly Glu Glu Phe Tyr Glu Ala Ser Pro
145 150 155 160
Tyr Glu Pro Val Thr Ser Arg Leu Ser Asp Ile Phe Arg Leu Ala Ser
165 170 175
Ile Phe Ser Gly Thr Gly Thr Asp Pro Ala Val Ser Thr Lys Ser Asn
180 185 190
His Cys Leu Asp Ala Ala Lys Ala Cys Asn Leu Asn Asp Asn Cys Lys
195 200 205
Lys Leu Arg Ser Ser Tyr Ile Ser Ile Cys Asn Arg Glu Ile Ser Pro
210 215 220
Thr Glu Arg Cys Asn Arg Arg Lys Cys His Lys Ala Leu Arg Gln Phe
225 230 235 240
Phe Asp Arg Val Pro Ser Glu Tyr Thr Tyr Arg Met Leu Phe Cys Ser
245 250 255
Cys Gln Asp Gln Ala Cys Ala Glu Arg Arg Arg Gln Thr Ile Leu Pro
260 265 270

Ser Cys Ser Tyr Glu Asp Lys Glu Lys Pro Asn Cys Leu Asp Leu Arg
275 280 285
Ser Leu Cys Arg Thr Asp His Leu Cys Arg Ser Arg Leu Ala Asp Phe
290 295 300
His Ala Asn Cys Arg Ala Ser Tyr Arg Thr Ile Thr Ser Cys Pro Ala
305 310 315 320
Asp Asn Tyr Gln Ala Cys Leu Gly Ser Tyr Ala Gly Met Ile Gly Phe
325 330 335
Asp Met Thr Pro Asn Tyr Val Asp Ser Asn Pro Thr Gly Ile Val Val
340 345 350
Ser Pro Trp Cys Asn Cys Arg Gly Ser Gly Asn Met Glu Glu Glu Cys
355 360 365
Glu Lys Phe Leu Arg Asp Phe Thr Glu Asn Pro Cys Leu Arg Asn Ala
370 375 380
Ile Gln Ala Phe Gly Asn Gly Thr Asp Val Asn Met Ser Pro Lys Gly
385 390 395 400
Pro Ser Leu Pro Ala Thr Gln Ala Pro Arg Val Glu Lys Thr Pro Ser
405 410 415
Leu Pro Asp Asp Leu Ser Asp Ser Thr Ser Leu Gly Thr Ser Val Ile
420 425 430
Thr Thr Cys Thr Ser Ile Gln Glu Gln Gly Leu Lys Ala Asn Asn Ser
435 440 445
Lys Glu Leu Ser Met Cys Phe Thr Glu Leu Thr Thr Asn Ile Ile Pro
450 455 460
Gly Trp Arg Ala Trp Val Pro Val Val Leu Gly Val Leu Thr Ala Leu
465 470 475 480
Val Thr Ala Ala Ala Leu Ala Leu Ile Leu Leu Arg Lys Arg Arg Lys
485 490 495
Glu Thr Arg Phe Gly Gln Ala Phe Asp Ser Val Met Ala Arg Gly Glu
500 505 510
Pro Ala Val His Phe Arg Ala Ala Arg Ser Phe Asn Arg Glu Arg Pro
515 520 525
Glu Arg Ile Glu Ala Thr Leu Asp Ser Leu Gly Ile Ser Asp Glu Leu
530 535 540
Lys Glu Lys Leu Glu Asp Val Leu Ile Pro Glu Gln Gln Phe Thr Leu
545 550 555 560
Gly Arg Met Leu Gly Lys Gly Glu Phe Gly Ser Val Arg Glu Ala Gln
565 570 575
Leu Lys Gln Glu Asp Gly Ser Phe Val Lys Val Ala Val Lys Met Leu
580 585 590
Lys Ala Asp Ile Ile Ala Ser Ser Asp Ile Glu Glu Phe Leu Arg Glu
595 600 605
Ala Ala Cys Met Lys Glu Phe Asp His Pro His Val Ala Lys Leu Val
610 615 620
Gly Val Ser Leu Arg Ser Arg Ala Lys Gly Arg Leu Pro Ile Pro Met
625 630 635 640
Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ala Phe Leu Leu
645 650 655
Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln Thr Leu
660 665 670
Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr Leu Ser Ser
675 680 685
Arg Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Ala
690 695 700
Glu Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Arg Lys Ile
705 710 715 720
Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Cys Ala Ser Lys Leu Pro Val

725	730	735	
Lys Trp Leu Ala Leu Glu Ser Leu Ala Asp Asn Leu Tyr Thr Val Gln			
740	745	750	
Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Met Thr Arg			
755	760	765	
Gly Gln Thr Pro Tyr Ala Gly Ile Glu Asn Ala Glu Ile Tyr Asn Tyr			
770	775	780	
Leu Ile Gly Gly Asn Arg Leu Lys Gln Pro Pro Glu Cys Met Glu Asp			
785	790	795	800
Val Tyr Asp Leu Met Tyr Gln Cys Trp Ser Ala Asp Pro Lys Gln Arg			
805	810	815	
Pro Ser Phe Thr Cys Leu Arg Met Glu Leu Glu Asn Ile Leu Gly Gln			
820	825	830	
Leu Ser Val Leu Ser Ala Ser Gln Asp Pro Leu Tyr Ile Asn Ile Glu			
835	840	845	
Arg Ala Glu Glu Pro Thr Ala Gly Gly Ser Leu Glu Leu Pro Gly Arg			
850	855	860	
Asp Gln Pro Tyr Ser Gly Ala Gly Asp Gly Ser Gly Met Gly Ala Val			
865	870	875	880
Gly Gly Thr Pro Ser Asp Cys Arg Tyr Ile Leu Thr Pro Gly Gly Leu			
885	890	895	
Ala Glu Gln Pro Gly Gln Ala Glu His Gln Pro Glu Ser Pro Leu Asn			
900	905	910	
Glu Thr Gln Arg Leu Leu Leu Leu Gln Gln Gly Leu Leu Pro His Ser			
915	920	925	
Ser Cys Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg			
930	935	940	
Gly Lys Asp Leu Pro Val Leu			
945	950		

<210> 20
 <211> 888
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Chimeric receptor comprising murine sequence.

<400> 20			
Met Gly Gly Thr Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val			
1	5	10	15
Ile Val Gly Leu His Gly Val Arg Gly Lys Tyr Ala Leu Ala Asp Ala			
20	25	30	
Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro			
35	40	45	
Val Leu Asp Gln Leu Leu Glu Ala Gly Asn Ser Leu Ala Thr Glu Asn			
50	55	60	
Arg Phe Val Asn Ser Cys Thr Gln Ala Arg Lys Lys Cys Glu Ala Asn			
65	70	75	80
Pro Ala Cys Lys Ala Ala Tyr Gln His Leu Gly Ser Cys Thr Ser Ser			
85	90	95	
Leu Ser Arg Pro Leu Pro Leu Glu Glu Ser Ala Met Ser Ala Asp Cys			
100	105	110	
Leu Glu Ala Ala Glu Gln Leu Arg Asn Ser Ser Leu Ile Asp Cys Arg			
115	120	125	
Cys His Arg Arg Met Lys His Gln Ala Thr Cys Leu Asp Ile Tyr Trp			

130	135	140	
Thr Val His Pro Ala Arg Ser	Leu Gly Asp Tyr	Glu Leu Asp Val Ser	
145	150	155	160
Pro Tyr Glu Asp Thr Val	Thr Ser Lys Pro	Trp Lys Met Asn	Leu Ser
165	170	175	
Lys Leu Asn Met	Leu Lys Pro Asp	Ser Asp Leu Cys	Leu Lys Phe Ala
180	185	190	
Met Leu Cys Thr Leu His Asp	Lys Cys Asp Arg	Leu Arg Lys Ala Tyr	
195	200	205	
Gly Glu Ala Cys Ser	Gly Ile Arg Cys	Gln Arg His	Leu Cys Leu Ala
210	215	220	
Gln Leu Arg Ser Phe	Phe Glu Lys Ala	Ala Glu Ser His	Ala Gln Gly
225	230	235	240
Leu Leu Leu Cys Pro	Cys Pro Pro	Glu Asp Ala	Gly Cys Gly Glu Arg
245	250	255	
Arg Arg Asn Thr Ile Ala Pro	Ser Cys Ala	Leu Pro Ser Val	Thr Pro
260	265	270	
Asn Cys Leu Asp Leu Arg	Ser Phe Cys Arg	Ala Asp Pro	Leu Cys Arg
275	280	285	
Ser Arg Leu Met Asp Phe	Gln Thr His Cys	His Pro Met Asp	Ile Leu
290	295	300	
Gly Thr Cys Ala Thr Glu	Gln Ser Arg Cys	Leu Arg Ala Tyr	Leu Gly
305	310	315	320
Leu Ile Gly Thr Ala Met	Thr Pro Asn Phe	Ile Ser Lys Val	Asn Thr
325	330	335	
Thr Val Ala Leu Ser Cys	Thr Cys Arg	Gly Ser Gly Asn	Leu Gln Asp
340	345	350	
Glu Cys Glu Gln Leu Glu	Arg Ser Phe Ser	Gln Asn Pro	Cys Leu Val
355	360	365	
Glu Ala Ile Ala Ala Lys	Met Arg Phe His	Arg Gln Leu Phe	Ser Gln
370	375	380	
Asp Trp Ala Asp Ser	Thr Phe Ser Val Val	Gln Gln Gln Asn	Ser Asn
385	390	395	400
Pro Ala Trp Arg Ala Trp	Val Pro Val Val	Leu Gly Val	Leu Thr Ala
405	410	415	
Leu Val Thr Ala Ala Ala	Leu Ile Leu Leu	Arg Lys Arg Arg	
420	425	430	
Lys Glu Thr Arg Phe	Gly Gln Ala Phe	Asp Ser Val Met	Ala Arg Gly
435	440	445	
Glu Pro Ala Val His Phe	Arg Ala Ala Arg	Ser Phe Asn Arg	Glu Arg
450	455	460	
Pro Glu Arg Ile Glu	Ala Thr Leu Asp	Ser Leu Gly Ile	Ser Asp Glu
465	470	475	480
Leu Lys Glu Lys Leu	Glu Asp Val Leu	Ile Pro Glu Gln	Gln Phe Thr
485	490	495	
Leu Gly Arg Met	Leu Gly Lys	Glu Phe Gly Ser	Val Arg Glu Ala
500	505	510	
Gln Leu Lys Gln Glu	Asp Gly Ser	Phe Val Lys Val	Ala Val Lys Met
515	520	525	
Leu Lys Ala Asp Ile	Ile Ala Ser Ser	Asp Ile Glu	Glu Phe Leu Arg
530	535	540	
Glu Ala Ala Cys Met	Lys Glu Phe	Asp His Pro His	Val Ala Lys Leu
545	550	555	560
Val Gly Val Ser	Leu Arg Ser Arg	Ala Lys Gly Arg	Leu Pro Ile Pro
565	570	575	
Met Val Ile Leu Pro	Phe Met Lys His	Gly Asp Leu His	Ala Phe Leu
580	585	590	

Leu Ala Ser Arg Ile Gly Glu Asn Pro Phe Asn Leu Pro Leu Gln Thr
 595 600 605
 Leu Ile Arg Phe Met Val Asp Ile Ala Cys Gly Met Glu Tyr Leu Ser
 610 615 620
 Ser Arg Asn Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu
 625 630 635 640
 Ala Glu Asp Met Thr Val Cys Val Ala Asp Phe Gly Leu Ser Arg Lys
 645 650 655
 Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln Gly Cys Ala Ser Lys Leu Pro
 660 665 670
 Val Lys Trp Leu Ala Leu Glu Ser Leu Ala Asp Asn Leu Tyr Thr Val
 675 680 685
 Gln Ser Asp Val Trp Ala Phe Gly Val Thr Met Trp Glu Ile Met Thr
 690 695 700
 Arg Gly Gln Thr Pro Tyr Ala Gly Ile Glu Asn Ala Glu Ile Tyr Asn
 705 710 715 720
 Tyr Leu Ile Gly Gly Asn Arg Leu Lys Gln Pro Pro Glu Cys Met Glu
 725 730 735
 Asp Val Tyr Asp Leu Met Tyr Gln Cys Trp Ser Ala Asp Pro Lys Gln
 740 745 750
 Arg Pro Ser Phe Thr Cys Leu Arg Met Glu Leu Glu Asn Ile Leu Gly
 755 760 765
 Gln Leu Ser Val Leu Ser Ala Ser Gln Asp Pro Leu Tyr Ile Asn Ile
 770 775 780
 Glu Arg Ala Glu Glu Pro Thr Ala Gly Gly Ser Leu Glu Leu Pro Gly
 785 790 795 800
 Arg Asp Gln Pro Tyr Ser Gly Ala Gly Asp Gly Ser Gly Met Gly Ala
 805 810 815
 Val Gly Gly Thr Pro Ser Asp Cys Arg Tyr Ile Leu Thr Pro Gly Gly
 820 825 830
 Leu Ala Glu Gln Pro Gly Gln Ala Glu His Gln Pro Glu Ser Pro Leu
 835 840 845
 Asn Glu Thr Gln Arg Leu Leu Leu Gln Gln Gly Leu Leu Pro His
 850 855 860
 Ser Ser Cys Ala Asp Ala Ser Leu Lys Met Ala Asp Pro Asn Arg Phe
 865 870 875 880
 Arg Gly Lys Asp Leu Pro Val Leu
 885

<210> 21
 <211> 37
 <212> DNA
 <213> Homo sapiens

<400> 21
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37

<210> 22
 <211> 20
 <212> DNA
 <213> Mus musculus

<400> 22
 gccccgcgacc tccactgctg

20

<210> 23

<211> 18
<212> DNA
<213> *Mus musculus*

<400> 23
ctgtggggag cggccggcg

18

<210> 24
<211> 20
<212> DNA
<213> *Mus musculus*

<400> 24
cctgaaccta tggtaactgg

20

<210> 25
<211> 17
<212> DNA
<213> *Mus musculus*

<400> 25
acccagtcct ccctacc

17